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Gene Section
Short Communication

CBLc (Cas-Br-M (murine) ecotropic retroviral transforming sequence c)

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Identity

Other names: CBL-3

HGNC (Hugo): CBLC

Location : 19q13.2

DNA/RNA

Transcription

2.8-3 kb mRNA; 1422 bp open reading frame.

Protein

Description

474 amino acids; 52.5 kDa; the CBLc protein contains the evolutionarily conserved aminoterminal phosphotyrosine binding region and the Ring finger with a Cys3HisCys4 motif found in CBL and CBLb. The phosphotyrosine binding domain is composed of three interacting domains: a four-helix bundle (4H), an EF-hand calcium binding domain, and a divergent SH2 domain; the three domains together form an integrated phosphoprotein-recognition module; the CBLc protein lacks the extensive proline-rich domain and the leucine zipper found in CBL and CBLb; only one proline-rich motif is conserved at the carboxy terminus of CBLc; thus, CBLc structurally most resembles the C.elegans and D.melanogaster CBL-related proteins, SLI-1 and D-CBL, respectively; an alternatively spliced mRNA codes form a CBLc isoform lacking a critical region in the phosphotyrosine binding domain.

Expression

The CBLc gene is ubiquitously expressed with highest expression in the aerodigestive tract (stomach, liver, pancreas, small intestine, colon, trachea, and lung), prostate, thyroid gland, adrenal gland, and salivary gland.

Localisation

Cytoplasmic.

Function

Regulation of signal transduction pathways; CBLc is recruited to the EGF (epidermal growth factor) receptor (EGFR) upon EGF stimulation and inhibits EGF stimulated MAP kinase activation.

Mutations

Note

No genomic alterations described to date.

References

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